

(sample of submitted file)

## Structure Explorer - 1RYP

**Title** Crystal Structure Of The 20S Proteasome From Yeast At 2.4 Angstroms Resolution  
**Classification** Multicatalytic Proteinase  
**Compound** Mol\_Id: 1; Molecule: 20S Proteasome; Chain: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U, V, W, X, Y, Z, 1, 2; Ec: 3.4.99.46; Mutation: Chains H, V, T1A, Chain L, Z, K33R; Biological\_Unit: Yeast Proteasome Seems To Be Composed Of 14 Different Subunits Which Form A Highly Ordered Ring-Shaped Structure  
**Exp. Method** X-ray Diffraction

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Summary InformationView StructureDownload/Display FileStructural NeighborsGeometryOther SourcesSequence Details

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HEADER MULTICATALYTIC PROTEINASE 26-FEB-97 1RY  
TITLE CRYSTAL STRUCTURE OF THE 20S PROTEASOME FROM YEAST AT 2  
TITLE 2 ANGSTROMS RESOLUTION  
COMPND MOL\_ID: 1;  
COMPND 2 MOLECULE: 20S PROTEASOME;  
COMPND 3 CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P,  
COMPND 4 R, S, T, U, V, W, X, Y, Z, 1, 2;  
COMPND 5 EC: 3.4.99.46;  
COMPND 6 MUTATION: CHAINS H, V, T1A, CHAIN L, Z, K33R;  
COMPND 7 BIOLOGICAL\_UNIT: YEAST PROTEASOME SEEMS TO BE COMPOSED  
COMPND 8 14 DIFFERENT SUBUNITS WHICH FORM A HIGHLY ORDERED  
COMPND 9 RING-SHAPED STRUCTURE  
SOURCE MOL\_ID: 1;  
SOURCE 2 ORGANISM\_SCIENTIFIC: SACCHAROMYCES CEREVISIAE;  
SOURCE 3 ORGANISM\_COMMON: BAKER'S YEAST  
KEYWDS MULTICATALYTIC PROTEINASE, 20S PROTEASOME, PROTEIN  
KEYWDS 2 DEGRADATION, ANTIGEN PROCESSING, HYDROLASE, PROTEASE  
EXPDTA X-RAY DIFFRACTION  
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JRNAL TITL STRUCTURE OF 20S PROTEASOME FROM YEAST AT 2.4  
JRNAL TITL 2 RESOLUTION  
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REMARK 1  
REMARK 2  
REMARK 2 RESOLUTION. 1.9 ANGSTROMS.  
REMARK 3  
REMARK 3 REFINEMENT.  
REMARK 3 PROGRAM : X-PLOR 3.1  
REMARK 3 AUTHORS : BRUNGER  
REMARK 3  
REMARK 3 DATA USED IN REFINEMENT.  
REMARK 3 RESOLUTION RANGE HIGH (ANGSTROMS) : 1.9  
REMARK 3 RESOLUTION RANGE LOW (ANGSTROMS) : 50.  
REMARK 3 DATA CUTOFF (SIGMA(F)) : 2.  
REMARK 3 DATA CUTOFF HIGH (ABS(F)) : 100000000.  
REMARK 3 DATA CUTOFF LOW (ABS(F)) : 0.1  
REMARK 3 COMPLETENESS (WORKING+TEST) (%) : 90.5  
REMARK 3 NUMBER OF REFLECTIONS : 752101  
REMARK 3  
REMARK 3 FIT TO DATA USED IN REFINEMENT.  
REMARK 3 CROSS-VALIDATION METHOD : NULL